

Result No.	Score	Match	Length	DB	ID	Description
1	1373	100.0	1373	9	US-10-978-203-3	Sequence 3, Appl
2	1373	100.0	1373	9	US-10-978-131-3	Sequence 3, Appl
3	1345.8	98.0	1364	3	US-09-822-849A-19	Sequence 19, Appl
4	1320.2	96.2	1353	6	US-10-210-951-3	Sequence 3, Appl
5	1320.2	96.2	1353	6	US-10-211-884-3	Sequence 3, Appl
6	1320.2	96.2	1353	6	US-10-211-858-3	Sequence 3, Appl
7	1285	93.6	1306	5	US-10-272-411-16	Sequence 16, Appl
8	1285	93.6	1306	5	US-10-218-547-23	Sequence 23, Appl
9	1285	93.6	1306	5	US-10-272-328A-16	Sequence 16, Appl
10	1285	93.6	1306	6	US-10-310-793-29	Sequence 29, Appl
11	1285	93.6	1306	7	US-10-202-062-23	Sequence 23, Appl
12	1285	93.6	1306	8	US-10-825-282-19	Sequence 19, Appl
13	1285	93.6	1306	10	US-11-028-780-23	Sequence 23, Appl
14	629.2	45.8	898	3	US-09-742-454A-1	Sequence 1, Appl
15	629.2	45.8	898	3	US-09-883-777-1	Sequence 1, Appl
16	629.2	45.8	898	8	US-10-754-847-1	Sequence 1, Appl
17	629.2	45.8	898	9	US-10-898-575-1	Sequence 1, Appl
18	629.2	45.8	898	9	US-10-971-250-1	Sequence 1, Appl
19	614.6	44.8	1168	9	US-10-978-203-1	Sequence 1, Appl
20	614.6	44.8	1168	9	US-10-978-131-1	Sequence 1, Appl
21	445.4	32.4	493	3	US-09-918-995-21225	Sequence 21225, A
22	281	20.5	408	3	US-09-960-352-2197	Sequence 2197, A
23	193.4	14.1	1395	3	US-09-878-134-66	Sequence 66, Appl

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	372.6	27.1	584	12	US-11-136-527-3597	Sequence 3597, Ap
2	372.6	27.1	584	12	US-11-136-527-7693	Sequence 7693, Ap
3	51.2	3.7	2028	8	US-10-821-234-359	Sequence 359, App
4	51.2	3.7	2336	9	US-11-072-512-1925	Sequence 1925, Ap
5	48.6	3.5	415117	8	US-10-995-561-13274	Sequence 13274, A
C 6	48	3.5	405	6	US-09-925-065A-572785	Sequence 572785, A
7	47.8	3.5	6360	12	US-11-056-470-2	Sequence 2, Appli
8	47.8	3.5	100000	12	US-11-124-367A-5048	Sequence 5048, Ap
9	47.6	3.5	1055	12	US-11-154-257-1	Sequence 1, Appli
10	47.6	3.5	5706	12	US-11-052-554A-519	Sequence 519, App
C 11	47.6	3.5	6590	12	US-11-000-688-609	Sequence 609, App
C 12	47.2	3.4	76427	12	US-11-124-367A-5041	Sequence 5041, Ap
C 13	47	3.4	607	6	US-09-925-065A-878733	Sequence 878733, A
C 14	46.8	3.4	466	6	US-09-925-065A-337232	Sequence 337232, A
C 15	46.8	3.4	176771	7	US-10-330-773-143	Sequence 143, App
C 16	46	3.4	1557	8	US-10-996-217A-6	Sequence 6, Appli
17	46	3.4	170995	12	US-11-121-086-35	Sequence 35, Appl
18	46	3.4	241805	8	US-10-995-561-13215	Sequence 13215, A
19	45.8	3.3	607	6	US-09-925-065A-507181	Sequence 507181, A
20	45.4	3.3	607	6	US-09-925-065A-878734	Sequence 878734, A

	Query Match	27.1%	Score 372.6	DB 12	Length 584
	Best Local Similarity	79.9%	Pred. No. 1.1e-79		
	Matches 465	Conservative 0	Mismatches 107	Indels 10	Gaps 2
QY	448	CCACGACCTGGGACGACGACGAGCGACGAGGAGGTGTGGACGGGACAGTCACTGCTGGGAG	507		
Db	2	CNACAGCCAGGACAGGATGGAGCACAGGACAGGTGTGGATGGGACAGTGAAGTCTGGGAA	61		
QY	508	GAAGCCGAGATCAACAGCTTCCAGCCCTCTCGCTACACCGCCAGATCGGGGAGTTTATA	567		

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OM protein - protein search, using sw model

Run on: March 1, 2006, 22:37:13 ; Search time 164 Seconds  
(without alignments)  
723.558 Million cell updates/sec

Title: US-09-245-198A-4  
Perfect score: 1444  
Sequence: 1 MSLLDPEISARRLPLPSLGS.....PWAHLKAAPFTYFGLFQVH 284

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA Main:
- 1: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubaa/US08\_PUBCOMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubaa/US09\_PUBCOMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubaa/US10A\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1444	100.0	284	5	US-10-978-203-4
2	1444	100.0	284	5	US-10-978-131-4
3	1268	87.8	249	3	US-09-905-810-2
4	1268	87.8	249	3	US-09-782-980-44
5	1268	87.8	249	4	US-10-218-547-24
6	1268	87.8	249	4	US-10-210-951-4
7	1268	87.8	249	4	US-10-211-884-4
8	1268	87.8	249	4	US-10-710-793-30
9	1268	87.8	249	4	US-10-211-858-4
10	1268	87.8	249	4	US-10-202-062-24
11	1268	87.8	249	4	US-10-806-018-44
12	1268	87.8	249	5	US-10-825-282-20
13	1268	87.8	249	5	US-10-916-141-2
14	1268	87.8	249	6	US-11-028-780-24
15	1066	73.8	273	3	US-09-743-454A-2
16	1066	73.8	273	3	US-09-883-777-2
17	1066	73.8	273	5	US-10-754-847-2
18	1066	73.8	273	5	US-10-898-575-2
19	1066	73.8	273	5	US-10-971-250-2
20	1020	70.6	225	3	US-09-905-810-1
21	1020	70.6	225	5	US-10-916-141-1
22	1020	70.6	225	5	US-10-978-203-2
23	1020	70.6	225	5	US-10-978-131-2
24	731	50.6	141	5	US-10-778-890-11
25	504	34.9	98	4	US-10-338-083-14
26	504	34.9	98	4	US-10-611-399-14
27	504	34.9	98	5	US-10-794-751-14

28	116	8.0	325	6	US-11-097-143-29451	Sequence 29451, A
29	116	8.0	409	3	US-09-813-329-6	Sequence 6, Appli
30	116	8.0	409	6	US-11-142-736-6	Sequence 6, Appli
31	114	7.9	166	5	US-10-739-930-8217	Sequence 8217, Ap
32	108.5	7.5	211	4	US-10-218-654-70	Sequence 70, Appl
33	108.5	7.5	211	4	US-10-262-439-70	Sequence 70, Appl
34	108.5	7.5	260	4	US-10-218-654-65	Sequence 65, Appl
35	108.5	7.5	260	4	US-10-262-439-65	Sequence 65, Appl
36	106.5	7.4	254	4	US-10-218-547-18	Sequence 18, Appl
37	106.5	7.4	254	4	US-10-310-793-24	Sequence 24, Appl
38	106.5	7.4	254	4	US-10-420-050-4	Sequence 4, Appli
39	106.5	7.4	254	4	US-10-202-062-18	Sequence 18, Appl
40	106.5	7.4	254	4	US-10-408-765A-509	Sequence 509, App
41	106.5	7.4	254	4	US-10-646-308-16	Sequence 16, Appl
42	106.5	7.4	254	4	US-10-756-783-2	Sequence 2, Appli
43	106.5	7.4	254	4	US-10-428-181A-181	Sequence 181, App
44	106.5	7.4	254	5	US-10-756-149-5150	Sequence 5150, Ap
45	106.5	7.4	254	6	US-11-028-780-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-10-978-203-4  
; Sequence 4, Application US/10978203  
; Publication No. US20050112666A1  
; GENERAL INFORMATION:  
; APPLICANT: Chicheportiche, Yves  
; TITLE OF INVENTION: Tumor Necrosis Factor Related Ligand  
; FILE REFERENCE: A003  
; CURRENT APPLICATION NUMBER: US/10/978, 203  
; CURRENT FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: 60/023,541  
; PRIOR FILING DATE: 1996-08-07  
; PRIOR APPLICATION NUMBER: 60/028,515  
; PRIOR FILING DATE: 1996-10-18  
; PRIOR APPLICATION NUMBER: 60/040,820  
; PRIOR FILING DATE: 1997-03-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 284  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-10-978-203-4

Query Match 100.0%; Score 1444; DB 5; Length 284;  
Best Local Similarity 100.0%; Pred. No. 4.3e-117;  
Matches 284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSLLDPEISARRLPLPSLGSRDGAVRQAPPAPMAARRSQRGRGEGTALLVPLA	60
Db	1	MSLLDPEISARRLPLPSLGSRDGAVRQAPPAPMAARRSQRGRGEGTALLVPLA	60
Qy	61	LGGLALACLGLLAVVSLGSRASLSAQEPABELVAEBDDPSELNPQTEESQDPAPFL	120
Db	61	LGGLALACLGLLAVVSLGSRASLSAQEPABELVAEBDDPSELNPQTEESQDPAPFL	120
Qy	121	NRLVRRPSAPKGRKTRARAAIAAHYVHPRPDGAGVDTGTVSGWEARINSSSPLR	180
Db	121	NRLVRRPSAPKGRKTRARAAIAAHYVHPRPDGAGVDTGTVSGWEARINSSSPLR	180
Qy	181	YNRQIGSFIVTRAGLYLYCQVHFDEGKAVYLLDLVDCGLALRCLSEFSATASLSGP	240
Db	181	YNRQIGSFIVTRAGLYLYCQVHFDEGKAVYLLDLVDCGLALRCLSEFSATASLSGP	240
Qy	241	QLRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPFLTYFGLFQVH	284
Db	241	QLRLCQVSGLLALRPGSSLRIRTLPAWHLKAAPFLTYFGLFQVH	284

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OM protein - protein search, using sw model

Run on: March 1, 2006, 22:37:53 ; Search time 21 Seconds  
(without alignments)  
269.766 Million cell updates/sec

Title: US-09-245-198a-4  
Perfect score: 1444  
Sequence: 1 MSLLDFEISARELPLPSRLG.....PWAHLKAAPFLTYGLFQVH 284

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 133702 seqs, 19947517 residues

Total number of hits satisfying chosen parameters: 133702

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*

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- 2: /cgm2\_6/ptodata/1/pubaa/US06\_NEW\_PUB.pep.\*
- 3: /cgm2\_6/ptodata/1/pubaa/US07\_NEW\_PUB.pep.\*
- 4: /cgm2\_6/ptodata/1/pubaa/PCT\_NEW\_PUB.pep.\*
- 5: /cgm2\_6/ptodata/1/pubaa/US03\_NEW\_PUB.pep.\*
- 6: /cgm2\_6/ptodata/1/pubaa/US10\_NEW\_PUB.pep.\*
- 7: /cgm2\_6/ptodata/1/pubaa/US11\_NEW\_PUB.pep.\*
- 8: /cgm2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	6.9	912	6	US-10-964-313-12
2	97	6.7	441	7	US-11-087-099-2892
3	93	6.4	810	6	US-10-954-468-37
4	92	6.4	240	6	US-10-987-663-6
5	92	6.4	240	7	US-11-136-341A-1
6	91.5	6.3	564	7	US-11-124-367A-263
7	89.5	6.2	616	6	US-10-858-730-21
8	89	6.2	316	7	US-11-032-797-4
9	89	6.2	316	7	US-11-238-266-2
10	89	6.2	564	7	US-11-087-099-3568
11	88.5	6.1	278	6	US-10-861-934-16
12	88.5	6.1	278	6	US-10-861-934-26
13	88.5	6.1	281	6	US-10-861-934-8
14	88.5	6.1	281	6	US-10-861-934-30
15	88.5	6.1	281	7	US-11-213-368-11
16	88.5	6.1	281	7	US-11-213-368-12
17	88.5	6.1	3073	7	US-11-143-980-50
18	87	6.0	291	7	US-11-032-797-5
19	87	6.0	427	7	US-11-156-084-350
20	86	6.0	241	7	US-11-084-647-5
21	84.5	5.9	367	6	US-10-131-826A-208
22	84.5	5.9	367	6	US-10-973-115B-208
23	84.5	5.9	377	7	US-11-087-099-12099
24	83	5.7	586	7	US-11-072-512-2947
25	82.5	5.7	204	7	US-11-136-341A-31

## ALIGNMENTS

### RESULT 1

US-10-964-313-12  
; Sequence 12, Application US/10964313  
; Publication No. US20050287629A1  
; GENERAL INFORMATION:  
; APPLICANT: GROZINGER, CHRISTINA M.  
; APPLICANT: HASSIG, CHRISTIAN A.  
; APPLICANT: SCHREIBER, STUART L.  
; TITLE OF INVENTION: CLASS II HUMAN HISTONE DEACETYLASES, AND USES RELATED  
; TITLE OF INVENTION: THERETO  
; FILE REFERENCE: HUV-037.02  
; CURRENT APPLICATION NUMBER: US/10/964,313  
; CURRENT FILING DATE: 2004-10-13  
; PRIOR APPLICATION NUMBER: 05/800,187  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/186,802  
; PRIOR FILING DATE: 2000-03-03  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 12  
; LENGTH: 912  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-964-313-12

Query Match 6.9%; Score 99; DB 6; Length 912;  
Best Local Similarity 24.2%; Pred. No. 0.55;  
Matches 46; Conservative 21; Mismatches 67; Indels 56; Gaps 6;  
QY 11 RLPLPRSLGSRDGGAVR-----QAQPPAPMAAR-----RSQRRGR- 47  
DB 361 RQIPSAEDLFTDGGPGQVDDGLEHRELHGQPEARGPAPLQHPQVLLWEQRLAGRL 420  
QY 48 -RCEPGTALLVPLALGLGIALACIGLLAVVLSGRSASLSAQBPQAEVLVABDDPSL 106  
DB 421 PRGSTGDTVLLPLAQGHRPLS-----RAQSSPAPASLSAPEPASQARVLSSETPART 475  
QY 107 NPQT-----BESQDP-----APPLNLRVPRRSAPKGRKTRAR 139  
DB 476 LPTTGLIYDVSVMKHKQCSGDNRRHPHAGRIQISWLSRQLRGLRSQCCLGRKASLE 535  
QY 140 RAIAAHYEVH 149  
DB 536 ELQSVHSERH 545

### RESULT 2

US-11-087-099-2892

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 2, 2006, 08:36:59 ; Search time 865 Seconds  
(without alignments)  
2715.033 Million cell updates/sec

Title: US-09-245-198a-4  
Perfect score: 1444  
Sequence: 1 MSLLDFEISARLPLPSLG.....PWAHLKAAPFTYGLFQVH 284

Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues  
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-MATRIX=blosom62 -TRANS=human4.0.cdi -LIST=45 -DOALIGN=ptco -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptco -NORM=ext  
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Database : Published Applications NA Main:

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- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1444	100.0	1373	9	US-10-978-203-3
2	1444	100.0	1373	9	US-10-978-131-3
3	1406	97.4	1364	3	US-09-822-849A-19
4	1366	94.6	1353	6	US-10-210-951-3
5	1366	94.6	1353	6	US-10-211-884-3
6	1366	94.6	1353	6	US-10-211-858-3
7	1298	89.9	1306	5	US-10-272-411-16
8	1298	89.9	1306	5	US-10-272-411-16

8	1298	89.9	1306	5	US-10-218-547-23	Sequence 23, Appl
9	1298	89.9	1306	5	US-10-272-328A-16	Sequence 16, Appl
10	1298	89.9	1306	6	US-10-310-793-29	Sequence 29, Appl
11	1298	89.9	1306	7	US-10-202-062-23	Sequence 23, Appl
12	1298	89.9	1306	8	US-10-825-282-19	Sequence 19, Appl
13	1298	89.9	1306	10	US-11-028-780-23	Sequence 23, Appl
14	1066	73.8	898	3	US-09-742-454A-1	Sequence 1, Appl
15	1066	73.8	898	3	US-09-883-777-1	Sequence 1, Appl
16	1066	73.8	898	8	US-10-754-847-1	Sequence 1, Appl
17	1066	73.8	898	9	US-10-898-575-1	Sequence 1, Appl
18	1066	73.8	898	9	US-10-971-250-1	Sequence 1, Appl
19	1020	70.6	1168	9	US-10-978-203-1	Sequence 1, Appl
20	1020	70.6	1168	9	US-10-978-131-1	Sequence 1, Appl
21	479	33.2	408	3	US-09-960-352-2197	Sequence 2197, Ap
22	137.5	9.5	135638	6	US-10-314-657-1	Sequence 1, Appl
23	137.5	9.5	135638	9	US-10-473-193-1	Sequence 1, Appl
24	133	9.2	1587	7	US-10-425-114-34084	Sequence 34084, A
25	132	9.1	1790	8	US-10-425-115-50959	Sequence 50959, A
26	129.5	9.0	264	3	US-09-983-965-2183	Sequence 2183, Ap
27	128.5	8.9	723	7	US-10-437-963-21510	Sequence 21510, A
28	126.5	8.8	1317	7	US-10-260-238-5494	Sequence 5494, Ap
29	126.5	8.8	1509	7	US-10-425-114-22810	Sequence 22810, A
30	126.5	8.8	1660	10	US-11-073-512-11	Sequence 11, Appl
31	125.5	8.7	2587	7	US-10-437-963-40736	Sequence 40736, A
32	125	8.7	1138	7	US-10-425-114-31500	Sequence 31500, A
33	125	8.7	1471	8	US-10-425-115-120811	Sequence 120811, A
34	124.5	8.6	2226	7	US-10-437-963-68385	Sequence 68385, A
35	124.5	8.6	2832	5	US-10-115-178-2	Sequence 2, Appl
36	124.5	8.6	154746	3	US-09-827-688-8	Sequence 8, Appl
37	124	8.6	3957	6	US-10-200-562-193	Sequence 193, App
38	124	8.6	3957	6	US-10-237-551-193	Sequence 193, App
39	124	8.6	3957	9	US-10-945-050-193	Sequence 193, App
40	124	8.6	18876	6	US-10-329-079-42	Sequence 42, Appl
41	124	8.6	61944	6	US-10-329-079-34	Sequence 34, Appl
42	124	8.6	154746	3	US-09-827-688-8	Sequence 8, Appl
43	122.5	8.5	9025608	6	US-10-156-761-1	Sequence 1, Appl
44	121.5	8.4	1830	7	US-10-437-963-16748	Sequence 16748, A
45	121.5	8.4	2741	7	US-10-437-963-102249	Sequence 102249, A

# ALIGNMENTS

RESULT 1  
US-10-978-203-3  
; Sequence 3, Application US/10978203  
; Publication No. US20050112666A1  
; GENERAL INFORMATION:  
; APPLICANT: Chicheportiche, Yves  
; APPLICANT: Browning, Jeffrey  
; TITLE OF INVENTION: Tumor Necrosis Factor Related Ligand  
; FILE REFERENCE: A003  
; CURRENT APPLICATION NUMBER: US/10/978,203  
; CURRENT FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: 60/023,541  
; PRIOR FILING DATE: 1996-08-07  
; PRIOR APPLICATION NUMBER: 60/028,515  
; PRIOR FILING DATE: 1996-10-18  
; PRIOR APPLICATION NUMBER: 60/040,820  
; PRIOR FILING DATE: 1997-03-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1373  
; TYPE: DNA  
; ORGANISM: homo sapien  
US-10-978-203-3

Alignment Scores:  
Pred. No.: 1.28e-154 Length: 1373  
Score: 1444.00 Matches: 284  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 2, 2006, 08:37:41 ; Search time 379 Seconds  
(without alignments)  
1642.836 Million cell updates/sec

Title: US-09-245-198A-4  
Perfect score: 1444  
Sequence: 1 MSLLDFEISARLLPLPSLG.....PWAHLKAAPFLTYGLFQVH 284

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7218512 seqs, 1096188070 residues

Total number of hits satisfying chosen parameters: 14437024

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abes/ABSWEB.spool/US09245198/runat\_01032006\_135043\_26897/app\_query.fasta.1  
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct-THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:

- 1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/PTC\_NEW\_PUB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
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- 7: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	652	45.2	584	12 US-11-136-527-3597	Sequence 3597, Ap
2	652	45.2	584	12 US-11-136-527-7693	Sequence 7693, Ap
3	118.5	8.2	1005	8 US-10-858-730-185	Sequence 185, App
4	117.5	8.1	3880	12 US-11-122-329-121	Sequence 121, App

c 5	117	8.1	11070	12	US-11-075-185-34	Sequence 34, Appl
c 6	117	8.1	78869	12	US-11-075-185-1	Sequence 1, Appl
c 7	115	8.0	1278	7	US-10-978-927-21	Sequence 21, Appl
c 8	115	8.0	1278	7	US-10-507-692-4	Sequence 4, Appl
c 9	115	8.0	1345	7	US-10-978-927-40	Sequence 40, Appl
c 10	115	8.0	4778	12	US-11-082-154A-70	Sequence 70, Appl
c 11	115	8.0	5510	8	US-11-082-154A-71	Sequence 71, Appl
c 12	115	8.0	5855	8	US-10-161-408-27	Sequence 27, Appl
c 13	115	8.0	5855	12	US-11-082-154A-112	Sequence 112, App
c 14	115	8.0	5855	12	US-11-082-154A-127	Sequence 127, App
c 15	115	8.0	6119	12	US-11-082-154A-126	Sequence 126, App
c 16	115	8.0	7600	12	US-11-082-154A-115	Sequence 115, App
c 17	115	8.0	7631	12	US-11-082-154A-116	Sequence 116, App
c 18	115	8.0	8521	12	US-11-082-154A-123	Sequence 123, App
c 19	115	8.0	8851	12	US-11-082-154A-124	Sequence 124, App
c 20	115	8.0	9080	12	US-11-082-154A-110	Sequence 110, App
c 21	115	8.0	10474	12	US-11-082-154A-125	Sequence 125, App
c 22	114.5	7.9	10524	12	US-11-075-185-37	Sequence 37, Appl
c 23	114	7.9	26757	12	US-11-124-367A-5102	Sequence 5102, Ap
c 24	114	7.9	40987	8	US-10-985-561-13503	Sequence 13503, A
c 25	114	7.9	67088	8	US-10-995-561-13365	Sequence 13365, A
c 26	111	7.7	1278	7	US-10-978-927-22	Sequence 22, Appl
c 27	111	7.7	1278	7	US-10-978-927-26	Sequence 26, Appl
c 28	111	7.7	1278	7	US-10-978-927-38	Sequence 38, Appl
c 29	110.5	7.7	153376	12	US-11-121-086-5	Sequence 5, Appl
c 30	110	7.6	613	6	US-09-925-065A-665469	Sequence 665469,
c 31	110	7.6	876	12	US-11-143-980-15	Sequence 15, Appl
c 32	110	7.6	2000	9	US-11-072-175-79	Sequence 79, Appl
c 33	110	7.6	2589	12	US-11-122-329-48	Sequence 48, Appl
c 34	110	7.6	4335	7	US-10-330-773-848	Sequence 848, App
c 35	110	7.6	116856	12	US-11-143-980-1	Sequence 1, Appl
c 36	109.5	7.6	613	6	US-09-925-065A-665468	Sequence 665468,
c 37	109.5	7.6	3121	8	US-10-964-313-11	Sequence 11, Appl
c 38	109	7.5	3250	12	US-11-156-953-1	Sequence 1, Appl
c 39	109	7.5	88421	9	US-11-205-109-1	Sequence 1, Appl
c 40	108.5	7.5	2895	12	US-11-245-147-225	Sequence 225, App
c 41	108.5	7.5	10968	12	US-11-075-185-35	Sequence 35, Appl
c 42	108.5	7.5	78869	12	US-11-075-185-1	Sequence 1, Appl
c 43	108	7.5	172543	12	US-11-121-086-6	Sequence 6, Appl
c 44	107.5	7.4	153376	12	US-11-121-086-5	Sequence 5, Appl
c 45	107.5	7.4	170995	12	US-11-121-086-35	Sequence 35, Appl

# ALIGNMENTS

RESULT 1

US-11-136-527-3597  
; Sequence 3597, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3597  
; LENGTH: 584  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
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; NAME/KEY: misc feature  
; LOCATION: (396)..(396)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (440)..(440)  
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